SEQUENCE LISTINGS

<110> INJE UNIVERSITY

<120> CANCER CELL TARGETING GENE DELIVERY METHOD

<130> Q94769

<150> KR 10-2003-0079897
<151> 1003-11-12

<150> PCT/KR2004/000545
<151> 2004-03-15

<160> 11

<170> KopatentIn 1.71

<210> 1
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Env F primer

<400> 1
cgcggatccg aattccatac ctggtgttgc tgacta 36

<210> 2
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> 597LN primer

<400> 2
agctggacct ggctgccacc acctccgcta ttttggtccc attttac 47

<210> 3
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> LC597 primer

<400> 3
caaccccgcc gcaggtggag gaggcagtga atggactcaa aaatttcaa 49

<210> 4
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Spike R2 primer

<400> 4
tgctctagaa ttcttaaagg ttaccttcgt tctct 35

<210> 5
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> LnkNScFv primer

<400> 5
ggaggtggtg gcagccaggt ccagctagtg cagtct 36

<210> 6
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> ScFvLnkC primer

<400> 6
actgcctcct ccacctgcgg cggggttgaa gtccca 36

<210> 7
<211> 2058
<212> DNA
<213> SEATO type of GaLV Env glycoprotein

<220>
<221> sig_peptide
<222> (1)..(126)

<220>
<221> misc_feature
<222> (127)..(1467)
<223> surface subunit region

<220>
<221> misc_feature
<222> (1468)..(2025)
<223> transmembrain domain

<400> 7
atggtattgc tgcctgggtc catgcttctc acctcaaacc tgcaccacct tcggcaccag 60

atgagtcctg ggagctggaa aagactgatc atcctcttaa gctgcgtatt cggcggcggc 120

gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcaggtactg 180

tcccaaactg gagacgttgt ctgggataca aaggcagtcc agcccccttg gacttggtgg 240

cccacactta aacctgatgt atgtgccttg gcggctagtc ttgagtcctg ggatatcccg 300

ggaaccgatg tctcgtcctc taaacgagtc agacctccgg actcagacta tactgccgct 360

tataagcaaa tcacctgggg agccataggg tgcagctacc ctcgggctag gactagaatg 420

gcaagctcta ccttctacgt atgtccccgg gatggccgga ccctttcaga agctagaagg 480

tgcgggggc tagaatccct atactgtaaa gaatgggatt gtgagaccac ggggaccggt 540

tattggctat ctaaatcctc aaaagacctc ataactgtaa aatgggacca aaatagcgaa 600

tggactcaaa aatttcaaca gtgtcaccag accggctggt gtaacccct taaaatagat 660

ttcacagaca aaggaaaatt atccaaggac tggataacgg gaaaaacctg gggattaaga 720

ttctatgtgt ctggacatcc aggcgtacag ttcaccattc gcttaaaaat caccaacatg 780

ccagctgtgg cagtaggtcc tgacctcgtc cttgtggaac aaggacctcc tagaacgtcc 840

ctcgctctcc cacctcctct tcccccaagg gaagcgccac cgccatctct ccccgactct 900

aactccacag ccctggcgac tagtgcacaa actcccacgg tgagaaaaac aattgttacc 960

ctaaacactc cgcctcccac cacaggcgac agacttttg atcttgtgca gggggccttc 1020

ctaaccttaa atgctaccaa cccaggggcc actgagtctt gctggctttg tttggccatg 1080

ggcccccctt attatgaagc aatagcctca tcaggagagg tcgcctactc caccgacctt 1140

gaccggtgcc gctgggggac ccaaggaaag ctcaccctca ctgaggtctc aggacacggg 1200

ttgtgcatag gaaaggtgcc ctttacccat cagcatctct gcaatcagac cctatccatc 1260

aattcctccg gagaccatca gtatctgctc ccctccaacc atagctggtg ggcttgcagc 1320

actggcctca ccccttgcct ctccacctca gtttttaatc agactagaga tttctgtatc 1380

caggtccagc tgattcctcg catctattac tatcctgaag aagttttgtt acaggcctat 1440

gacaattctc accccaggac taaaagagag gctgtctcac ttaccctagc tgttttactg 1500

gggttgggaa tcacggcggg aataggtact ggttcaactg ccttaattaa aggacctata 1560

gacctccagc aaggcctgac aagcctccag atcgccatag atgctgacct ccgggccctc 1620

caagactcag tcagcaagtt agaggactca ctgacttccc tgtccgaggt agtgctccaa 1680

aataggagag gccttgactt gctgtttcta aaagaaggtg gcctctgtgc ggccctaaag 1740

gaagagtgct gtttttacat agaccactca ggtgcagtac gggactccat gaaaaaactc 1800

aaagaaaaac tggataaaag acagttagag cgccagaaaa gccaaaactg gtatgaagga 1860

tggttcaata actccccttg gttcactacc ctgctatcaa ccatcgctgg gcccctatta 1920

ctcctccttc tgttgctcat cctcgggcca tgcatcatca ataagttagt tcaattcatc 1980

aatgatagga taagtgcagt taaaattctg gtccttagac aaaaatatca ggccctagag 2040

aacgaaggta acctttaa 2058

<210> 8
<211> 786
<212> DNA
<213> Tag-72pS1

<220>
<221> misc_feature
<222> (346)..(390)
<223> (Gly4Ser)3 linker

<220>
<221> misc_feature
<222> (739)..(777)
<223> PreS1 Tag

<400> 8
caggtccagc tagtgcagtc tggggctgaa gtgaagaagc ctggggcttc agtgaaggtg 60

tcctgcaagg cttctggcta caccttcact gaccatgcaa ttcactgggt gcgccaggcc 120

cctggacaac gccttgagtg gatgggatat ttttctcctg gcaacgatga ttttaaatac 180

tcccagaagt tccagggacg cgtgacaatc actgcagaca aatccgcgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtct attactgtgc aagatcgttg 300

aacatggcat actggggcca agggactctg gtcactgtct cttcaggtgg aggcggttca 360

ggcggaggtg gctctggcgg tggcggatcg gacattgtga tgacccagtc tccagactcc 420

ctggctgtgt ctctgggcga gagggccacc atcaactgca agtccagcca gagtgtttta 480

tacagcagca acaataagaa ctacttagct tggtaccagc agaaaccagg acagcctcct 540

aagctgctca tttactgggc atctacccgg gaatccgggg tccctgaccg attcagtggc 600

agcgggtctg ggacagattt cactctcacc atcagcagcc tgcaggctga agatgtggca 660

gtttattact gtcagcaata ttattcctat ccgttgacgt tcggccaagg gaccaaggtg 720

gaaatcaaag cggccgcagg agccaacgca aacaatccag attgggactt caaccccgcc 780

gcatag 786

<210> 9
<211> 13
<212> PRT
<213> PreS1 epitope at C-terminal of Tag-72pS1

<400> 9
Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro
1 5 10

<210> 10
<211> 2871
<212> DNA
<213> Artificial Sequence

<220>
<223> ScFv-GaLV Env GP chimeric peptide (FvGEL199) DNA

<400> 10
atggtattgc tgcctgggtc catgcttctc acctcaaacc tgcaccacct tcggcaccag 60

atgagtcctg ggagctggaa aagactgatc atcctcttaa gctgcgtatt cggcggcggc 120

gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcaggtactg 180

tcccaaactg gagacgttgt ctgggataca aaggcagtcc agcccccttg gacttggtgg 240

cccacactta aacctgatgt atgtgccttg gcggctagtc ttgagtcctg ggatatcccg 300

ggaaccgatg tctcgtcctc taaacgagtc agacctccgg actcagacta tactgccgct 360

tataagcaaa tcacctgggg agccataggg tgcagctacc ctcgggctag gactagaatg 420

gcaagctcta ccttctacgt atgtccccgg gatggccgga ccctttcaga agctagaagg 480

tgcgggggc tagaatccct atactgtaaa gaatgggatt gtgagaccac ggggaccggt 540

tattggctat ctaaatcctc aaaagacctc ataactgtaa aatgggacca aaatagcgga 600

ggtggtggca gccaggtcca gctagtgcag tctggggctg aagtgaagaa gcctggggct 660

tcagtgaagg tgtcctgcaa ggcttctggc tacaccttca ctgaccatgc aattcactgg 720

gtgcgccagg cccctggaca acgccttgag tggatgggat atttttctcc tggcaacgat 780

gattttaaat actcccagaa gttccaggga cgcgtgacaa tcactgcaga caaatccgcg 840

agcacagcct acatggagct gagcagcctg agatctgagg acacggcggt ctattactgt 900

gcaagatcgt tgaacatggc atactggggc caagggactc tggtcactgt ctcttcaggt 960

ggaggcggtt caggcggagg tggctctggc ggtggcggat cggacattgt gatgacccag 1020

tctccagact ccctggctgt gtctctgggc gagagggcca ccatcaactg caagtccagc 1080

cagagtgttt tatacagcag caacaataag aactacttag cttggtacca gcagaaacca 1140

ggacagcctc ctaagctgct catttactgg gcatctaccc gggaatccgg ggtccctgac 1200

cgattcagtg gcagcgggtc tgggacagat ttcactctca ccatcagcag cctgcaggct 1260

gaagatgtgg cagtttatta ctgtcagcaa tattattcct atccgttgac gttcggccaa 1320

gggaccaagg tggaaatcaa agcggccgca ggagccaacg caaacaatcc agattgggac 1380

ttcaaccccg ccgcaggtgg aggaggcagt gaatggactc aaaaatttca acagtgtcac 1440

cagaccggct ggtgtaaccc ccttaaaata gatttcacag acaaaggaaa attatccaag 1500

gactggataa cgggaaaaac ctggggatta agattctatg tgtctggaca tccaggcgta 1560

cagttcacca ttcgcttaaa aatcaccaac atgccagctg tggcagtagg tcctgacctc 1620

gtccttgtgg aacaaggacc tcctagaacg tccctcgctc tcccacctcc tcttccccca 1680

agggaagcgc caccgccatc tctccccgac tctaactcca cagccctggc gactagtgca 1740

caaactccca cggtgagaaa aacaattgtt accctaaaca ctccgcctcc caccacaggc 1800

gacagacttt ttgatcttgt gcaggggggcc ttcctaacct taaatgctac caacccaggg 1860

gccactgagt cttgctggct ttgtttggcc atgggccccc cttattatga agcaatagcc 1920

tcatcaggag aggtcgccta ctccaccgac cttgaccggt gccgctgggg gacccaagga 1980

aagctcaccc tcactgaggt ctcaggacac gggttgtgca taggaaaggt gcccttacc 2040

catcagcatc tctgcaatca gaccctatcc atcaattcct ccggagacca tcagtatctg 2100

ctcccctcca accatagctg gtgggcttgc agcactggcc tcacccctg cctctccacc 2160

tcagttttta atcagactag agatttctgt atccaggtcc agctgattcc tcgcatctat 2220

tactatcctg aagaagtttt gttacaggcc tatgacaatt ctcaccccag gactaaaaga 2280

gaggctgtct cacttaccct agctgtttta ctggggttgg gaatcacggc gggaataggt 2340

actggttcaa ctgccttaat taaaggacct atagacctcc agcaaggcct gacaagcctc 2400

cagatcgcca tagatgctga cctccgggcc ctccaagact cagtcagcaa gttagaggac 2460

tcactgactt ccctgtccga ggtagtgctc caaaatagga gaggccttga cttgctgttt 2520

ctaaaagaag gtggcctctg tgcggcccta aaggaagagt gctgttttta catagaccac 2580

tcaggtgcag tacgggactc catgaaaaaa ctcaaagaaa aactggataa aagacagtta 2640

gagcgccaga aaagccaaaa ctggtatgaa ggatggttca ataactcccc ttggttcact 2700

accctgctat caaccatcgc tgggccccta ttactcctcc ttctgttgct catcctcggg 2760

ccatgcatca tcaataagtt agttcaattc atcaatgata ggataagtgc agttaaaatt 2820

ctggtcctta gacaaaaata tcaggcccta gagaacgaag gtaaccttta a 2871

<210> 11
<211> 956
<212> PRT
<213> Artificial Sequence

<220>
<223> ScFv-GaLV Env GP chimeric ligand (FvGEL199)

<400> 11

```
Met Val Leu Leu Pro Gly Ser Met Leu Leu Thr Ser Asn Leu His His
 1               5                  10                  15

Leu Arg His Gln Met Ser Pro Gly Ser Trp Lys Arg Leu Ile Ile Leu
            20                  25                  30

Leu Ser Cys Val Phe Gly Gly Gly Gly Thr Ser Leu Gln Asn Lys Asn
        35                  40                  45

Pro His Gln Pro Met Thr Leu Thr Trp Gln Val Leu Ser Gln Thr Gly
    50                  55                  60

Asp Val Val Trp Asp Thr Lys Ala Val Gln Pro Pro Trp Thr Trp Trp
65                  70                  75                  80

Pro Thr Leu Lys Pro Asp Val Cys Ala Leu Ala Ala Ser Leu Glu Ser
                85                  90                  95

Trp Asp Ile Pro Gly Thr Asp Val Ser Ser Ser Lys Arg Val Arg Pro
            100                 105                 110

Pro Asp Ser Asp Tyr Thr Ala Ala Tyr Lys Gln Ile Thr Trp Gly Ala
        115                 120                 125

Ile Gly Cys Ser Tyr Pro Arg Ala Arg Thr Arg Met Ala Ser Ser Thr
    130                 135                 140

Phe Tyr Val Cys Pro Arg Asp Gly Arg Thr Leu Ser Glu Ala Arg Arg
145                 150                 155                 160

Cys Gly Gly Leu Glu Ser Leu Tyr Cys Lys Glu Trp Asp Cys Glu Thr
                165                 170                 175
```

Thr Gly Thr Gly Tyr Trp Leu Ser Lys Ser Ser Lys Asp Leu Ile Thr
180 185 190

Val Lys Trp Asp Gln Asn Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
195 200 205

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
210 215 220

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Ala Ile His Trp
225 230 235 240

Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Phe Ser
245 250 255

Pro Gly Asn Asp Asp Phe Lys Tyr Ser Gln Lys Phe Gln Gly Arg Val
260 265 270

Thr Ile Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser
275 280 285

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu
290 295 300

Asp Met Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
305 310 315 320

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
325 330 335

Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg
340 345 350

Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn
355 360 365

Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
370 375 380

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
385 390 395 400

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser

405 410 415

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr
420 425 430

Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ala
435 440 445

Ala Ala Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro Ala
450 455 460

Ala Gly Gly Gly Gly Ser Glu Trp Thr Gln Lys Phe Gln Gln Cys His
465 470 475 480

Gln Thr Gly Trp Cys Asn Pro Leu Lys Ile Asp Phe Thr Asp Lys Gly
485 490 495

Lys Leu Ser Lys Asp Trp Ile Thr Gly Lys Thr Trp Gly Leu Arg Phe
500 505 510

Tyr Val Ser Gly His Pro Gly Val Gln Phe Thr Ile Arg Leu Lys Ile
515 520 525

Thr Asn Met Pro Ala Val Ala Val Gly Pro Asp Leu Val Leu Val Glu
530 535 540

Gln Gly Pro Pro Arg Thr Ser Leu Ala Leu Pro Pro Pro Leu Pro Pro
545 550 555 560

Arg Glu Ala Pro Pro Pro Ser Leu Pro Asp Ser Asn Ser Thr Ala Leu
565 570 575

Ala Thr Ser Ala Gln Thr Pro Thr Val Arg Lys Thr Ile Val Thr Leu
580 585 590

Asn Thr Pro Pro Pro Thr Thr Gly Asp Arg Leu Phe Asp Leu Val Gln
595 600 605

Gly Ala Phe Leu Thr Leu Asn Ala Thr Asn Pro Gly Ala Thr Glu Ser
610 615 620

Cys Trp Leu Cys Leu Ala Met Gly Pro Pro Tyr Tyr Glu Ala Ile Ala
625 630 635 640

Ser Ser Gly Glu Val Ala Tyr Ser Thr Asp Leu Asp Arg Cys Arg Trp
645 650 655

Gly Thr Gln Gly Lys Leu Thr Leu Thr Glu Val Ser Gly His Gly Leu
660 665 670

Cys Ile Gly Lys Val Pro Phe Thr His Gln His Leu Cys Asn Gln Thr
675 680 685

Leu Ser Ile Asn Ser Ser Gly Asp His Gln Tyr Leu Leu Pro Ser Asn
690 695 700

His Ser Trp Trp Ala Cys Ser Thr Gly Leu Thr Pro Cys Leu Ser Thr
705 710 715 720

Ser Val Phe Asn Gln Thr Arg Asp Phe Cys Ile Gln Val Gln Leu Ile
725 730 735

Pro Arg Ile Tyr Tyr Tyr Pro Glu Glu Val Leu Leu Gln Ala Tyr Asp
740 745 750

Asn Ser His Pro Arg Thr Lys Arg Glu Ala Val Ser Leu Thr Leu Ala
755 760 765

Val Leu Leu Gly Leu Gly Ile Thr Ala Gly Ile Gly Thr Gly Ser Thr
770 775 780

Ala Leu Ile Lys Gly Pro Ile Asp Leu Gln Gln Gly Leu Thr Ser Leu
785 790 795 800

Gln Ile Ala Ile Asp Ala Asp Leu Arg Ala Leu Gln Asp Ser Val Ser
805 810 815

Lys Leu Glu Asp Ser Leu Thr Ser Leu Ser Glu Val Val Leu Gln Asn
820 825 830

Arg Arg Gly Leu Asp Leu Leu Phe Leu Lys Glu Gly Gly Leu Cys Ala
835 840 845

Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ile Asp His Ser Gly Ala Val
850 855 860

Arg Asp Ser Met Lys Lys Leu Lys Glu Lys Leu Asp Lys Arg Gln Leu
865 870 875 880

Glu Arg Gln Lys Ser Gln Asn Trp Tyr Glu Gly Trp Phe Asn Asn Ser
885 890 895

Pro Trp Phe Thr Thr Leu Leu Ser Thr Ile Ala Gly Pro Leu Leu Leu
900 905 910

Leu Leu Leu Leu Leu Ile Leu Gly Pro Cys Ile Ile Asn Lys Leu Val
915 920 925

Gln Phe Ile Asn Asp Arg Ile Ser Ala Val Lys Ile Leu Val Leu Arg
930 935 940

Gln Lys Tyr Gln Ala Leu Glu Asn Glu Gly Asn Leu
945 950 955